EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	2	"20050130171"	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 10:17
S1	48395	bodary.in. or clark.in. or hunt.in. or jackman.in.	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 09:04
S2	3588	($array$2 or $5chipo$2 or immobili$) and S1	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 09:05
S3	1818588	($array$2 or $5chip$2 or immobili$)	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 09:06
S4	483	immune adj relate$ adj disorder	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 09:06
S5	10	S1 and S3 and S4	US-PGPUB; USPAT; USOCR; FPRS; EPO; JPO; DERWENT; IBM_TDB	OR	ON	2007/01/23 10:17

SCORE Search Results Details for Application 10527100 and Search Result 20070112_105344_us-10-527-100a-1.rng.

Score Home Page | Retrieve Application List | SCORE System Overview | SCORE FAQ | Comments / Suggestions

This page gives you Search Results detail for the Application 10527100 and Search Result 20070112_105344_us-10-527-100a-1.rng.

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                          GenCore version 5.1.9
                    Copyright (c) 1993 - 2007  Biocceleration Ltd.


OM nucleic - nucleic search, using sw model

Run on:         January 12, 2007, 18:43:29 ; Search time 1280 Seconds
                                           (without alignments)
                                           10834.220 Million cell updates/sec

Title:          US-10-527-100A-1
Perfect score:  1989
Sequence:       1 ggcacgagggcgtcacgggc.....ttaaaaaaaaaaaaaaaaaa 1989

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters:      10489840

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        N_Geneseq_8:*
                 1:  geneseqn1980s:*
                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
                 6:  geneseqn2002as:*
                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:*
                 14:  geneseqn2005s:*
                 15:  geneseqn2006s:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1989	100.0	1989	12	ADL91486	Adl91486 Human imm
2		1975	99.3	3425	14	ADY20185	Ady20185 DNA encod
3		1973.4	99.2	2834	12	ADI61675	Adi61675 Human cDN
4		1973.4	99.2	2834	14	AEA43840	Aea43840 Human cDN
5		1939	97.5	2032	10	ADD29570	Add29570 Human tum
6		1939	97.5	2032	10	ADA53766	Ada53766 Human cod
7		1930	97.0	2000	6	ABQ60910	Abq60910 Clone IMA
8		1741.8	87.6	1911	13	ACN39899	Acn39899 Tumour-as
9	c	1359.6	68.4	149480	6	ABL61947	Abl61947 Colon ade
10	c	1359.6	68.4	149480	6	ABL68365	Abl68365 Kidney ca
11	c	1359.6	68.4	149480	6	ABL61948	Abl61948 Colon ade
12		762.4	38.3	1162	8	ABZ57031	Abz57031 Human kin
13	c	664.8	33.4	854	13	ADR26106	Adr26106 Breast ca
14	c	642.2	32.3	819	14	AEB35205	Aeb35205 Human Gef
15		597	30.0	2971	5	AAS84667	Aas84667 DNA encod
16		517	26.0	590	9	ACH40628	Ach40628 Human foe
17		479	24.1	1181	4	AAS27166	Aas27166 cDNA enco
18		479	24.1	1181	4	ABK43848	Abk43848 DNA encod
19		479	24.1	1181	5	AAS34308	Aas34308 Human cDN
20		479	24.1	1181	10	ADB93344	Adb93344 Human cDN
21		479	24.1	1181	12	ADI54235	Adi54235 cDNA enco
22		465	23.4	518	9	ACH38122	Ach38122 Human end
23		372.6	18.7	445	9	ACH41694	Ach41694 Human foe
24		318.8	16.0	636	5	AAS84665	Aas84665 DNA encod
25		263.6	13.3	600	14	AEE14026	Aee14026 Hamster c
26		261.4	13.1	586	14	AEE17668	Aee17668 Hamster S
27		258.4	13.0	274	2	AAT24451	Aat24451 Human gen
28		203	10.2	277	13	ADU10968	Adu10968 Solid tum
29		122.6	6.2	560	12	ACH74342	Ach74342 Human gen
30		115	5.8	115	12	ACH88042	Ach88042 Human gen
31		107.8	5.4	452	5	AAS84666	Aas84666 DNA encod
32		89	4.5	129	3	AAC14427	Aac14427 Human sec
33		74.2	3.7	6036	12	ADM66990	Adm66990 Human hom
34		74.2	3.7	6050	13	ACN40874	Acn40874 Tumour-as
35		74.2	3.7	6170	5	AAS44966	Aas44966 cDNA enco
36		74.2	3.7	6351	5	AAS45154	Aas45154 cDNA enco
37		74.2	3.7	6573	10	ADI60598	Adi60598 Secreted
38		74.2	3.7	8977	10	ADE48299	Ade48299 Human MIC
39		72.6	3.7	4327	13	ADR06825	Adr06825 Full leng
40	c	70	3.5	2000	8	ADA71938	Ada71938 Rice gene
41		70	3.5	3827	12	ADM66989	Adm66989 Murine ad
42		68.8	3.5	428	8	ABX53847	Abx53847 Bovine ES
43		58.2	2.9	1869	13	ADR07616	Adr07616 Full leng
44		58.2	2.9	2134	3	AAA08112	Aaa08112 Human bla
45		58.2	2.9	2224	10	ADC32017	Adc32017 Human nov

ALIGNMENTS

<!--StartFragment-->RESULT 3
ADI61675
ID ADI61675 standard; cDNA; 2834 BP.
XX
AC ADI61675;
XX
DT 22-APR-2004 (first entry)
XX
DE Human cDNA downregulated in Alzheimer's disease, INCYTE 001697.5.
XX
KW Human; ss; Alzheimer's disease; differential display; neuroprotective;
KW brain disorder.
XX
OS Homo sapiens.
XX
PN US6682888-B1.
XX
PD 27-JAN-2004.
XX
PF 05-MAY-2000; 2000US-00566921.
XX
PR 05-MAY-2000; 2000US-00566921.
XX
PA (INCY-) INCYTE CORP.
XX
PI Loring JF, Tingley DW, Edwards CM;
XX
DR WPI; 2004-118572/12.
XX
PT New composition comprising cDNAs that are differentially expressed in
PT brain disorders, useful for diagnosing or treating Alzheimer's disease.
XX
PS Claim 1; SEQ ID NO 43; 223pp; English.
XX
CC The invention relates to a new composition comprising ADI61633-
CC ADI61770and their complements that are cDNAs differentially expressed in
CC brain disorders. Also included are a high throughput method for detecting
CC differential expression of one or more cDNAs in a sample containing
CC nucleic acids and a high throughput method for screening a library of
CC molecules or compounds to identify a ligand that specifically binds a
CC cDNA. The expression of the each of the cDNAs is downregulated at least
CC two-fold in the brain of the subjects with Alzheimer's disease (ADI61633-
CC ADI61727) or upregulated at least two fold in Alzheimer's disease
CC (ADI61728-ADI61770). The composition is useful for diagnosing or treating
CC Alzheimer's disease. The present sequence is a cDNA downregulated at
CC least two-fold in the brain of the subjects with Alzheimer's disease.
XX
SQ Sequence 2834 BP; 708 A; 759 C; 763 G; 604 T; 0 U; 0 Other;

Query Match 99.2%; Score 1973.4; DB 12; Length 2834;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1974; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         10 GCGTCACGGGCGCCCGGCCCGTTAAAACGCTGCTGGCTGGAGCCACCTCCCTCCCTGCAG 69
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        519 GCGTCACGGGCGCCCGGCCCGTTAAAACGCTGCTGGCTGGAGCCACCTCCCTCCCTGCAG 578

Qy         70 CCCGCAACGGGAATGGAGTAAAGGGAGACCCGTCGACCTGGCCACGGGGATCAGCGATGG 129
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        579 CCCGCAACGGGAATGGAGTAAAGGGAGACCCGTCGACCTGGCCACGGGGATCAGCGATGG 638
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Qy       130 AATTAAAGCAATCTTTGTCCACCCATCTGGAAGCCGAGAAGCCTCTGAGGCGCTATGGGG 189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       639 AATTAAAGCAATCTTTGTCCACCCATCTGGAAGCCGAGAAGCCTCTGAGGCGCTATGGGG 698

Qy       190 CGGTGGAGGAGACGGCTTGGAAAACGGAGAGACTGGGGAGAAATCAGCTGGACATCATCT 249
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       699 CGGTGGAGGAGACGGCTTGGAAAACGGAGAGACTGGGGAGAAATCAGCTGGACATCATCT 758

Qy       250 CCATGGCGGAGACAACCATGATGCCAGAGGAGATTGAGCTGGAGATGGCAAAAATTCAGC 309
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       759 CCATGGCGGAGACAACCATGATGCCAGAGGAGATTGAGCTGGAGATGGCAAAAATTCAGC 818

Qy       310 GTCTCCGGGAAGTCTTGGTCCGCCGGGAGTCTGAGCTCAGGTTCATGATGGATGACATCC 369
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       819 GTCTCCGGGAAGTCTTGGTCCGCCGGGAGTCTGAGCTCAGGTTCATGATGGATGACATCC 878

Qy       370 AGCTCTGCAAGGACATCATGGACTTGAAGCAGGAGCTGCAGAACTTGGTCGCCATCCCAG 429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       879 AGCTCTGCAAGGACATCATGGACTTGAAGCAGGAGCTGCAGAACTTGGTCGCCATCCCAG 938

Qy       430 AAAAAGAAAAAACCAAACTGCAGAAGCAGAGAGAGGATGAGCTAATCCAGAAGATCCACA 489
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       939 AAAAAGAAAAAACCAAACTGCAGAAGCAGAGAGAGGATGAGCTAATCCAGAAGATCCACA 998

Qy       490 AACTGGTGCAGAAGAGAGACTTCCTGGTGGACGATGCGGAGGTCGAGCGGTTAAGGGAGC 549
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       999 AACTGGTGCAGAAGAGAGACTTCCTGGTGGACGATGCGGAGGTCGAGCGGTTAAGGGAGC 1058

Qy       550 AAGAAGAAGACAAGGAAATGGCTGATTTCCTGAGAATCAAGTTAAAACCTCTAGACAAAG 609
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1059 AAGAAGAAGACAAGGAAATGGCTGATTTCCTGAGAATCAAGTTAAAACCTCTAGACAAAG 1118

Qy       610 TAACCAAATCTCCAGCCAGCTCCCGGGCAGAGAAGAAAGCAGAGCCCCCACCTAGCAAGC 669
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1119 TAACCAAATCTCCAGCCAGCTCCCGGGCAGAGAAGAAAGCAGAGCCCCCACCTAGCAAGC 1178

Qy       670 CCACGGTGGCCAAGACGGGGCTGGCACTGATCAAGGATTGTTGCGGGGCCACCCAGTGCA 729
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db      1179 CCACGGTGGCCAAGACGGGGCTGGCATTGATCAAGGATTGTTGCGGGGCCACCCAGTGCA 1238

Qy       730 ACATCATGTAGCCCCCACGTGGGGTGCCCTGGGCCATGGGGACCCCCCCCCCACCCTCTTG 789
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1239 ACATCATGTAGCCCCCACGTGGGGTGCCCTGGGCCATGGGGACCCCCCCCCCACCCTCTTG 1298

Qy       790 TCTTTATAGCCCCCATTTCACCGGGGCCCAAGAGCTCTCCAAGGCAGAAGGGGTTGAAGG 849
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1299 TCTTTATAGCCCCCATTTCACCGGGGCCCAAGAGCTCTCCAAGGCAGAAGGGGTTGAAGG 1358

Qy       850 CAAGCCCGTGACTGTCACCAGAGGCCATGGGCACGGCAGGCGGGCCTGGCCACCCTGTAC 909
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1359 CAAGCCCGTGACTGTCACCAGAGGCCATGGGCACGGCAGGCGGGCCTGGCCACCCTGTAC 1418

Qy       910 AGAGTGTAGCAGTAGGGAGTCTCTCACCGTCGCATGGTCCTCCCCAGAGCATGCCGAACC 969
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1419 AGAGTGTAGCAGTAGGGAGTCTCTCACCGTCGCATGGTCCTCCCCAGAGCATGCCGAACC 1478

Qy       970 CAGGAGTCTGTCTCACTGTTTATCCAAACACCAGGAAAGGTCCTCCCTCAAAAAAGCATA 1029
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1479 CAGGAGTCTGTCTCACTGTTTATCCAAACACCAGGAAAGGTCCTCCCTCAAAAAAGCATA 1538

Qy      1030 TCTCCACTTCTCTCTAGCTGTATCTAACCCACCGTGTGAATGAACTGGGAGAGGGGCATG 1089
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1539 TCTCCACTTCTCTCTAGCTGTATCTAACCCACCGTGTGAATGAACTGGGAGAGGGGCATG 1598

Qy        1090 CTCCCCAGCTGTGTGTAGTCGTGACTTCTCAACAATCTAGCACCATGTCGGACACGTTCC 1149
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1599 CTCCCCAGCTGTGTGTAGTCGTGACTTCTCAACAATCTAGCACCATGTCGGACACGTTCC 1658

Qy        1150 CCATCCACCCTCCTAGCTCTGCTCTCAGAGCTAGGCACATGGGCACAGGTCCCCTCCCGT 1209
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1659 CCATCCACCCTCCTAGCTCTGCTCTCAGAGCTAGGCACATGGGCACAGGTCCCCTCCCGT 1718

Qy        1210 CTGTCCTCTCCCAGCAACTGTGCCCTGGAGGGCTCCACATGGCCCCCGTGTCTCTCGGGC 1269
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Db        1719 CTGTCCTCTCCCAGCAACTGTGCCCTGGAGGGCTCCACATGGCCCCCGTGTCTCTCGGGC 1778

Qy        1270 ACCACCCATATAGCAGTCCCAGAGGGCCCATCTGTAAAGATCGAGCTTGTGTGTGGTGTC 1329
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Db        1779 ACCACCCATATAGCAGTCCCAGAGGGCCCATCTGTAAAGATCGAGCTTGTGTGTGGTGTC 1838

Qy        1330 GTGGTCACATCTCCCGCTTCCCCCCATCCTGTGTCTGGGCACAGTTCACATCAGGACAGC 1389
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Db        1839 GTGGTCACATCTCCCGCTTCCCCCCATCCTGTGTCTGGGCACAGTTCACATCAGGACAGC 1898

Qy        1390 GTCCATTGTGCTCTCAGTCTGCCTCAGGTGTGTGCCTGGAGGGGGCCTGGACTGGCATGG 1449
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1899 GTCCATTGTGCTCTCAGTCTGCCTCAGGTGTGTGCCTGGAGGGGGCCTGGACTGGCATGG 1958

Qy        1450 ATCCAGTGTGCAGAAGAGCCAGCAGGGAACCGGAAGCTCTGATGTCAAGGCCAGAGCAGT 1509
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1959 ATCCAGTGTGCAGAAGAGCCAGCAGGGAACCGGAAGCTCTGATGTCAAGGCCAGAGCAGT 2018

Qy        1510 TGAGAATGGGACCCAGAGTAGATGCTGACCTGGGCACTCCACCATTCCGGGGCCACCACA 1569
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2019 TGAGAATGGGACCCAGAGTAGATGCTGACCTGGGCACTCCACCATTCCGGGGCCACCACA 2078

Qy        1570 GAGATGCCAGCAGGATGCCACTTTGCCAGCCCGACACACGGACCTTTGTAAAGAACAGCA 1629
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2079 GAGATGCCAGCAGGATGCCACTTTGCCAGCCCGACACACGGACCTTTGTAAAGAACAGCA 2138

Qy        1630 ACAGGCAGGAGAGGCAGCGTGTGACCAGATTGTGTCCCGTCATTGGGTGGCATATGTTAA 1689
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Db        2139 ACAGGCAGGAGAGGCAGCGTGTGACCAGATTGTGTCCCGTCATTGGGTGGCATATGTTAA 2198

Qy        1690 CTAGCTGCCAAACAACTTCAACCCGTGTAATTCATGTACATTTGCAACAGCCAGCCCGGT 1749
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Db        2199 CTAGCTGCCAAACAACTTCAACCCGTGTAATTCATGTACATTTGCAACAGCCAGCCCGGT 2258

Qy        1750 ACAGCCTGTGTGACTTCTCTGTATGTGTGTGTGTGTCGTGACCAGCCTAAGTAGTTAGCA 1809
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2259 ACAGCCTGTGTGACTTCTCTGTATGTGTGTGTGTGTCGTGACCAGCCTAAGTAGTTAGCA 2318

Qy        1810 TAACTCAAGATGCTGATGTGCAGTCACCCATCAGAGAAAATAAAAATGGAAACCACGTTC 1869
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Db        2319 TAACTCAAGATGCTGATGTGCAGTCACCCATCAGAGAAAATAAAAATGGAAACCACGTTC 2378

Qy        1870 ACAGCATTTTAAAAGTTTTTACTTTTTTTCTTGATTATGGAAGTAATCCATGTACATAGT 1929
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2379 ACAGCATTTTAAAAGTTTTTACTTTTTTTCTTGATTATGGAAGTAATCCATGTACATAGT 2438

Qy        1930 AAATCATTTTAAAAGTACAAAAAGTATGAAGAAGTTTGTCTTAAAAAAAAAAAAA 1984
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        2439 AAATCATTTTAAAAGTACAAAAAGTATGAAGAAGTTTGTCTTAAAAAAAAAAAAA 2493

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